

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: RABIN, Mark B.
- (ii) TITLE OF INVENTION: MUTATIONS IN THE BRCA1 GENE
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Howrey & Simon
  - (B) STREET: 1299 Pennsylvania Avenue, N.W.
  - (C) CITY: Washington
  - (D) STATE: District of Columbia
  - (E) COUNTRY: USA
  - (F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: Windows
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 09/038,946
  - (B) FILING DATE: March 12, 1998
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER:
  - (B) FILING DATE:

- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Halluin, Albert P.
  - (B) REGISTRATION NUMBER: 25,227
  - (C) REFERENCE/DOCKET NUMBER: 05371.0032.999

- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 202-383-7073
  - (B) TELEFAX: 202-383-6610
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5711 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCTCGCTGA	GACTTCCTGG	ACCCCGCACC	AGGCTGTGGG	GTTTCTCAGA	TAACTGGGC	60
CCIGCGCTCA	GGAGGCCTTC	ACCCCTCTGCT	CTGGGTAAG	TTCATTGAA	CAGAAAGAAA	120
TGGATTTATC	TGCTCTTCGC	GTTGAAGAAG	TACAAAATGT	CATTAATGCT	ATGCAGAAA	180
TCTTAGAGTG	TCCCCATCTGT	CTGGAGTTGA	TCAAGGAACC	TGTCTCCACA	AACTGTGACC	240
ACATATTTG	CAAATTTGC	ATGCTGAAAC	TTCTCAACCA	GAAGAAAGGG	CCTTCACAGT	300
GTCCTTTATG	TAAGAATGAT	ATAACCAAAA	GGAGCCTACA	AGAAAAGTACG	AGATTTAGTC	360
AACTTGTGA	AGAGCTATTG	AAAATCATTT	GTGCTTTCA	GCTTGACACCA	GGTTTGGAGT	420
ATGCAAACAG	CTATAATTTC	GCAAAAAAGG	AAAATAACTC	TCCTGAACAT	CTAAAAGATG	480
AAGTTTCTAT	CATCCAAAGT	ATGGGCTACA	GAAACCGTGC	CAAAGACTT	CTACAGAGTG	540
ACCCGAAAA	TCCTTCCTTG	CAGGAAACCA	GTCTCAGTGT	CCAACCTCTCT	AACCTTGGAA	600
CTGTGAGAAC	TCTGAGGACA	AAGCAGCGGA	TACAACCTCA	AAAGACGTCT	GTCTACATG	660
AATTGGGATC	TGATTCTCT	GAAGATCGG	TTAATTAGGC	AACTTATTGCG	AGTGTGGGAG	720
ATCAAGAATT	GTTACAATTC	ACCCCTCAAG	GAACCAGGGA	TGAAATCAGT	TTGGATTCTG	780
CAAAAAGGC	TGCTTGTGAA	TTTCTGAGA	CGGATGTAAC	AAATACTGAA	CATCATCAAC	840
CCAGTAATAA	TGATTTGAAC	ACCACTGAGA	AGCGTGCAGC	TGAGAGGCAT	CCAGAAAAGT	900
ATCAGGGTAG	TTCTGTTCA	AACTTGCATG	TGGAGCCATG	TGGCACAAAT	ACTCATGCCA	960
GCTCATTACA	GCATGAGAAC	AGCAGTTAT	TACTCACTAA	AGACAGAATG	AATGTAGAAA	1020
AGGCTGAATT	CTGTAATAAA	AGCAAACAGC	CTGGCTTAGC	AAGGAGCCAA	CATAACAGAT	1080
GGGCTGGAAG	TAAGGAAACA	TGTAATGATA	GGCGGACTCC	CAGCACAGAA	AAAAGGTAG	1140
ATCTGAATGC	TGATCCCCTG	TGTGAGAGAA	AAGAATGGAA	TAAGCAGAAA	CTGCCATGCT	1200
CAGAGAATCC	TAGAGATACT	GAAGATGTC	CTTGGATAAC	ACTAAATAGC	AGCATTGAGA	1260
AAAGTTAATGA	GTGGTTTCC	AGAAGTGATG	AACTGTTAGG	TTCTGATGAC	TCACATGATG	1320
GGGAGTCTGA	ATCAAATGCC	AAAGTAGCTG	ATGTATTGGA	CGTTCTAAAT	GAGGTAGATG	1380
AATATTCTGG	TTCTTCAGAG	AAAATAGACT	TACTGGCCAG	TGATCCTCAT	GAGGCTTTAA	1440
TATGTAAGAAG	TGAAAGAGTT	CACTCCAAAT	CACTAGAGAG	TAATATTGAA	GACAAAATAT	1500
TTGGGAAACAC	CTATCGAAG	AAGGCAAGCC	TCCCCAACTT	AAGGATGTA	ACTGAAAATC	1560
TAATTATAGG	AGCATTGTT	ACTGAGCCAC	AGATAATACA	AGAGCGTCCC	CTCACAAATA	1620
AATTAAAGCG	TAAAAGGAGA	CCTACATCAG	GCCTTCATCC	TGAGGATTTT	ATCAAGAAG	1680
CAGATTGGC	AGTTCAAAG	ACTCCTGAAA	TGATAAAATCA	GGGAACTAAC	CAAACGGAGC	1740
AGAATGGTCA	AGTGATGAAT	ATTACTAATA	GTGGTCATGA	GAATAAAACA	AAAGGTGATT	1800
CTATTCAAGAA	TGAGAAAAAT	CCTAACCCAA	TAGAATCACT	CGAAAAAGAA	TCTGCTTTCA	1860
AAACGAAAGC	TGAACCTATA	AGCAGCAGTA	TAAGCAATAT	GGAACTCGAA	TTAAATATCC	1920
ACAATTCAAA	AGCACCTAAA	AAGAATAGGC	TGAGGAGGAA	GTCTTCTACC	AGGCATATTG	1980
ATGCGCTTGA	ACTAGTAGTC	AGTAGAAATC	TAAGCCCACC	TAATTGTACT	GAATTGCAA	2040
TTGATAGTTG	TTCTAGCAGT	GAAGAGATAA	AGAAAAAAAGA	GTACAACCAA	ATGCCAGTCA	2100
GGCACAGCAG	AAACCTACAA	CTCATGGAAG	GTAAAGAAC	TGCAACTGG	GCCAAGAAGA	2160
GTAACAAGCC	AAATGAACAG	ACAAGTAAA	GACATGACAG	TGATACTTTG	CCAGAGCTGA	2220
AGTTAACAAA	TGCACCTGGT	TCTTTACTA	AGTGTTCAAA	TACCACTGAA	CTTAAAGAAT	2280
TTGTCAATCC	TAGCCTTCCA	AGAGAAGAAA	AAGAAGAGAA	ACTAGAAACA	GTAAAGTGT	2340
CTAATAATGC	TGAAGACCCC	AAAGATCTCA	TGTTAACGTG	AGAAAGGGTT	TTGCAAACGT	2400
AAAGATCTGT	AGAGAGTAGC	AGTATTTCAC	TGGTACCTGG	TACTGATTAT	GGCACTCAGG	2460
AAAGTATCTC	GTTACTGGAA	GTAGCACTC	TAGGGAAAGG	AAAAACAGAA	CCAAATAAT	2520
GTGTGAGTC	GTGTGAGCA	TTTAAAACC	CCAAGGGACT	AATTCACTGGT	TGTTCCAAAG	2580
ATAATAGAAA	TGACACAGAA	GGCTTTAAGT	ATCCATTGGG	ACATGAAGTT	AACCACAGTC	2640
GGGAAACAAG	CATAGAAAATG	GAAGAAAGTG	AACTTGATGC	TCAGTATTTG	CAGAATACAT	2700
TCAAGGTTTC	AAAGCGCCAG	TCATTTGCTC	TGTTTTCAA	TCCAGGAAT	GCAGAAGAGG	2760
AATGTGCAAC	ATTCTCTGCC	CACTCTGGGT	CTTTAAAGAA	ACAAAGTCCA	AAAGTCACCT	2820
TTGAATGTGA	ACAAAAGGAA	AAAATCAAG	GAAAGAATGA	GTCTAATATC	AAGCCTGTAC	2880
AGACAGTTAA	TATCACTGCA	GGCTTTCTG	TGGTTGGTCA	GAAAGATAAG	CCAGTTGATA	2940
ATGCCAAATG	TAGTATCAAA	GGAGGCTCTA	GGTTTTGTCT	ATCATCTCAG	TTCAGAGGCA	3000
ACGAAACTGG	ACTCATTACT	CCAAATAAAC	ATGGACTTT	ACAAAACCCA	TATCGTATAC	3060
CACCACTTT	TCCCCATCAAG	TCATTTGTTA	AAACTAAATG	TAAGAAAAT	CTGCTAGAGG	3120
AAAACCTTG	GGAACATTCA	ATGTCACCTG	AAAGAGAAAT	GGGAAATGAG	AACATTCCAA	3180
GTACAGTGA	CACAATTAGC	CGTAATAACA	TTAGAGAAA	TGTTTTAAA	GGAGCCAGCT	3240
CAAGCAATAT	TAATGAAGTA	GGTCCAGTA	CTAATGAAGT	GGGCTCCAGT	ATTAATGAAA	3300

TAGGTTCCAG	TGATGAAAAC	ATTCAAGCAG	AACTAGGTAG	AAACAGAGGG	CCAAAATTGA	3360
ATGCTATGCT	TAGATTAGGG	GTTTTGCAAC	CTGAGGTCTA	TAAACAAAGT	CTTCCTGGAA	3420
GTAATTGAA	GCATCCTGAA	ATAAAAAGC	AAGAATATGA	AGAAGTAGTT	CAGACTGTTA	3480
ATACAGATT	CTCTCCATAT	CTGATTTCAG	ATAACTTAGA	ACAGCCTATG	GGAAGTAGTC	3540
ATGCATCTCA	GGTTTGTCT	GAGCACCTG	ATGACCTGTT	AGATGATGGT	GAAATAAAGG	3600
AAGATACTAG	TTTTGCTGAA	AATGACATTA	AGGAAAGTTC	TGCTGTTTT	AGCAAAAGCG	3660
TCCAGAGAGG	AGAGCTTAGC	AGGAGTCCTA	GCCCCTTCAC	CCATACACAT	TTGGCTCAGG	3720
GTTACCGAAG	AGGGGCCAAG	AAATTAGAGT	CCTCAGAAGA	GAACATTATCT	AGTGAGGATG	3780
AAGAGCTTCC	CTGCTTCAA	CACTTGTAT	TTGGTAAAGT	AAACAATATA	CCTTCTCAGT	3840
CTACTAGGCA	TAGCACCGTT	GCTACCGAGT	GTCTGTCTAA	GAACACAGAG	GAGAATTAT	3900
TATCATTGAA	GAATAGCTTA	AATGACTGCA	GTAACCAGGT	AATATTGGCA	AAGGCATCTC	3960
AGGAACATCA	CCTTAGTGAG	AAAACAAAAT	GTTCTGCTAG	CTTGTGTTCT	TCACAGTGCA	4020
GTGAATTGGA	AGACTTGACT	GCAAATACAA	ACACCCAGGA	TCCTTCTTG	ATTGGTTCTT	4080
CCAAACAAAT	GAGGCATCAG	TCTGAAAGCC	AGGGAGTGG	TCTGAGTGAC	AAGGAATTGG	4140
TTTCAGATGA	TGAAGAAAAGA	GGAACCGGGCT	TGGAAGAAAA	TAATCAAGAA	GAGCAAAGCA	4200
TGGATTCAA	CTTAGGTGAA	GCAGCATCTG	GGTGTGAGAG	TGAAACAAGC	GTCTCTGAAG	4260
ACTGCTCAGG	GCTATCCTCT	CAGAGTGACA	TTTAACACAC	TCAGCAGAGG	GATACCATGC	4320
AAACATAACCT	GATAAAGCTC	CAGCAGGAAA	TGGCTGAAC	AGAAGCTGTG	TTAGAACAGC	4380
ATGGGAGCCA	GCCTTCTAAC	AGCTACCCCTT	CCATCATAAG	TGACTCCTCT	GCCCCTGAGG	4440
ACCTGCGAAA	TCCAGAACAA	AGCACATCAG	AAAAGCAGT	ATTAACCTCA	CAGAAAAGTA	4500
GTGAATACCC	TATAAGCCAG	AATCCAGAAG	GCCTTCTGTC	TGACAAGTT	GAGGTGCTG	4560
CAGATAGTT	TACCAAGAAA	AATAAAGAAC	CAGGAGTGG	AAGGTCAATCC	CCTTCTAAAT	4620
GCCCCATCATT	AGATGATAGG	TGGTACATGC	ACAGTTGCTC	TGGGAGTCTT	CAGAATAGAA	4680
ACTACCCATC	TCAAGAGGGAG	CTCATTAAGG	TTGTTGATGT	GGAGGAGCAA	CAGCTGGAAG	4740
AGTCTGGGCC	ACACGATTTG	ACGGAAACAT	CTTACTTGCC	AAGGCAAGAT	CTAGAGGGAA	4800
CCCCTTACCT	GGAAATCTGGA	ATCAGCCTCT	TCTCTGATGA	CCCTGAATCT	GATCCTCTG	4860
AAGACAGAGC	CCCAGAGTCA	GCTCGTGTG	GCAACATACC	ATCTTCAACC	TCTGCATTGA	4920
AAGTCCCCCA	ATTGAAAGTT	GCAGAACTCTG	CCCAGGGTCC	AGCTGCTGCT	CATACTACTG	4980
ATACTGCTGG	GTATAATGCA	ATGGAAGAAA	GTGTGAGCAG	GGAGAAGCCA	GAATTGACAG	5040
CTTCAACAGA	AAGGGTCAAC	AAAAGAATGT	CCATGGTGGT	GTCCTGGCCTG	ACCCCAGAAG	5100
AATTATGCT	CGTGTACAAG	TTTGCAGAA	AACACCAT	CACTTTAACT	AATCTAATT	5160
CTGAAGAGAC	TACTCATGTT	GTATGAAAAA	CAGATGCTGA	TTTGTGTTG	GAACGGACAC	5220
TGAAATATT	TCTAGGAATT	GGGGAGGAA	AATGGGTAGT	TAGCTATTTC	TGGGTGACCC	5280
AGTCTATTAA	AGAAAGAAAA	ATGCTGAATG	AGCATGATTT	TGAAGTCAGA	GGAGATGTGG	5340
TCAATGGAAG	AAACCACCAA	GGTCCAAAGC	GAGCAAGAGA	ATCCCAGGAC	AGAAAGATCT	5400
TCAGGGGGCT	AGAAATCTGT	TGCTATGGGC	CCTTCACCAA	CATGCCACAA	GATCAACTGG	5460
AATGGATGGT	ACAGCTGTGT	GGTGCTTCTG	TGGTGAAGGA	GCTTCATCA	TTCACCCCTG	5520
GCACAGGTGT	CCACCCAATT	GGGGTTGTGC	AGCCAGATGC	CTGGACAGAG	GACAATGGCT	5580
TCCATGCAAT	TGGGCAGATG	TGTGAGGCAC	CTGTTGTGAC	CCGAGAGTGG	GTGTTGGACA	5640
GTGTAGCACT	CTACCAAGTGC	CAGGAGCTGG	ACACCTACCT	GATACCCAG	ATCCCCACAA	5700
CCCACTACTG	A					5711

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1863 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val Gln Asn Val Ile Asn  
                   1               5               10               15  
  Ala Met Gln Lys Ile Leu Glu Cys Pro Ile Cys Leu Glu Leu Ile Lys

20	25	30
Glu Pro Val Ser Thr Lys Cys Asp His Ile Phe Cys Lys Phe Cys Met		
35	40	45
Leu Lys Leu Leu Asn Gln Lys Lys Gly Pro Ser Gln Cys Pro Leu Cys		
50	55	60
Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser		
65	70	75
Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp		
85	90	95
Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn		
100	105	110
Asn Ser Pro Glu His Leu Lys Asp Glu Val Ser Ile Ile Gln Ser Met		
115	120	125
Gly Tyr Arg Asn Arg Ala Lys Arg Leu Leu Gln Ser Glu Pro Glu Asn		
130	135	140
Pro Ser Leu Gln Glu Thr Ser Leu Ser Val Gln Leu Ser Asn Leu Gly		
145	150	155
Thr Val Arg Thr Leu Arg Thr Lys Gln Arg Ile Gln Pro Gln Lys Thr		
165	170	175
Ser Val Tyr Ile Glu Leu Gly Ser Asp Ser Ser Glu Asp Thr Val Asn		
180	185	190
Lys Ala Thr Tyr Cys Ser Val Gly Asp Gln Glu Leu Leu Gln Ile Thr		
195	200	205
Pro Gln Gly Thr Arg Asp Glu Ile Ser Leu Asp Ser Ala Lys Lys Ala		
210	215	220
Ala Cys Glu Phe Ser Glu Thr Asp Val Thr Asn Thr Glu His His Gln		
225	230	235
Pro Ser Asn Asn Asp Leu Asn Thr Thr Glu Lys Arg Ala Ala Glu Arg		
245	250	255
His Pro Glu Lys Tyr Gln Gly Ser Ser Val Ser Asn Leu His Val Glu		
260	265	270
Pro Cys Gly Thr Asn Thr His Ala Ser Ser Leu Gln His Glu Asn Ser		
275	280	285
Ser Leu Leu Leu Thr Lys Asp Arg Met Asn Val Glu Lys Ala Glu Phe		
290	295	300
Cys Asn Lys Ser Lys Gln Pro Gly Leu Ala Arg Ser Gln His Asn Arg		
305	310	315
Trp Ala Gly Ser Lys Glu Thr Cys Asn Asp Arg Arg Arg Thr Pro Ser Thr		
325	330	335
Glu Lys Lys Val Asp Leu Asn Ala Asp Pro Leu Cys Glu Arg Lys Glu		
340	345	350
Trp Asn Lys Gln Lys Leu Pro Cys Ser Glu Asn Pro Arg Asp Thr Glu		
355	360	365
Asp Val Pro Trp Ile Thr Leu Asn Ser Ser Ile Gln Lys Val Asn Glu		
370	375	380
Trp Phe Ser Arg Ser Asp Glu Leu Leu Gly Ser Asp Asp Ser His Asp		
385	390	395
Gly Glu Ser Glu Ser Asn Ala Lys Val Ala Asp Val Leu Asp Val Leu		
405	410	415
Asn Glu Val Asp Glu Tyr Ser Gly Ser Ser Glu Lys Ile Asp Leu Leu		
420	425	430
Ala Ser Asp Pro His Glu Ala Leu Ile Cys Lys Ser Glu Arg Val His		
435	440	445
Ser Lys Ser Val Glu Ser Asn Ile Glu Asp Lys Ile Phe Gly Lys Thr		
450	455	460
Tyr Arg Lys Lys Ala Ser Leu Pro Asn Leu Ser His Val Thr Glu Asn		
465	470	475
		480

Leu Ile Ile Gly Ala Phe Val Thr Glu Pro Gln Ile Ile Gln Glu Arg  
     485                          490                          495  
 Pro Leu Thr Asn Lys Leu Lys Arg Lys Arg Arg Pro Thr Ser Gly Leu  
     500                          505                          510  
 His Pro Glu Asp Phe Ile Lys Lys Ala Asp Leu Ala Val Gln Lys Thr  
     515                          520                          525  
 Pro Glu Met Ile Asn Gln Gly Thr Asn Gln Thr Glu Gln Asn Gly Gln  
     530                          535                          540  
 Val Met Asn Ile Thr Asn Ser Gly His Glu Asn Lys Thr Lys Gly Asp  
     545                          550                          555                          560  
 Ser Ile Gln Asn Glu Lys Asn Pro Asn Pro Ile Glu Ser Leu Glu Lys  
     565                          570                          575  
 Glu Ser Ala Phe Lys Thr Lys Ala Glu Pro Ile Ser Ser Ser Ile Ser  
     580                          585                          590  
 Asn Met Glu Leu Glu Leu Asn Ile His Asn Ser Lys Ala Pro Lys Lys  
     595                          600                          605  
 Asn Arg Leu Arg Arg Lys Ser Ser Thr Arg His Ile His Ala Leu Glu  
     610                          615                          620  
 Leu Val Val Ser Arg Asn Leu Ser Pro Pro Asn Cys Thr Glu Leu Gln  
     625                          630                          635                          640  
 Ile Asp Ser Cys Ser Ser Ser Glu Glu Ile Lys Lys Lys Tyr Asn  
     645                          650                          655  
 Gln Met Pro Val Arg His Ser Arg Asn Leu Gln Leu Met Glu Gly Lys  
     660                          665                          670  
 Glu Pro Ala Thr Gly Ala Lys Lys Ser Asn Lys Pro Asn Glu Gln Thr  
     675                          680                          685  
 Ser Lys Arg His Asp Ser Asp Thr Phe Pro Glu Leu Lys Leu Thr Asn  
     690                          695                          700  
 Ala Pro Gly Ser Phe Thr Lys Cys Ser Asn Thr Ser Glu Leu Lys Glu  
     705                          710                          715                          720  
 Phe Val Asn Pro Ser Leu Pro Arg Glu Glu Lys Glu Glu Lys Leu Glu  
     725                          730                          735  
 Thr Val Lys Val Ser Asn Asn Ala Glu Asp Pro Lys Asp Leu Met Leu  
     740                          745                          750  
 Ser Gly Glu Arg Val Leu Gln Thr Glu Arg Ser Val Glu Ser Ser Ser  
     755                          760                          765  
 Ile Ser Leu Val Pro Gly Thr Asp Tyr Gly Thr Gln Glu Ser Ile Ser  
     770                          775                          780  
 Leu Leu Glu Val Ser Thr Leu Gly Lys Ala Lys Thr Glu Pro Asn Lys  
     785                          790                          795                          800  
 Cys Val Ser Gln Cys Ala Ala Phe Glu Asn Pro Lys Gly Leu Ile His  
     805                          810                          815  
 Gly Cys Ser Lys Asp Asn Arg Asn Asp Thr Glu Gly Phe Lys Tyr Pro  
     820                          825                          830  
 Leu Gly His Glu Val Asn His Ser Arg Glu Thr Ser Ile Glu Met Glu  
     835                          840                          845  
 Glu Ser Glu Leu Asp Ala Gln Tyr Leu Gln Asn Thr Phe Lys Val Ser  
     850                          855                          860  
 Lys Arg Gln Ser Phe Ala Leu Phe Ser Asn Pro Gly Asn Ala Glu Glu  
     865                          870                          875                          880  
 Glu Cys Ala Thr Phe Ser Ala His Ser Gly Ser Leu Lys Lys Gln Ser  
     885                          890                          895  
 Pro Lys Val Thr Phe Glu Cys Glu Gln Lys Glu Glu Asn Gln Gly Lys  
     900                          905                          910  
 Asn Glu Ser Asn Ile Lys Pro Val Gln Thr Val Asn Ile Thr Ala Gly  
     915                          920                          925  
 Phe Pro Val Val Gly Gln Lys Asp Lys Pro Val Asp Asn Ala Lys Cys

930	935	940
Ser Ile Lys Gly Gly Ser Arg Phe Cys Leu Ser Ser Gln Phe Arg Gly		
945	950	955
Asn Glu Thr Gly Leu Ile Thr Pro Asn Lys His Gly Leu Leu Gln Asn		960
965	970	975
Pro Tyr Arg Ile Pro Pro Leu Phe Pro Ile Lys Ser Phe Val Lys Thr		
980	985	990
Lys Cys Lys Lys Asn Leu Leu Glu Glu Asn Phe Glu Glu His Ser Met		
995	1000	1005
Ser Pro Glu Arg Glu Met Gly Asn Glu Asn Ile Pro Ser Thr Val Ser		
1010	1015	1020
Thr Ile Ser Arg Asn Asn Ile Arg Glu Asn Val Phe Lys Gly Ala Ser		
1025	1030	1035
104		
Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu Val Gly Ser		
1045	1050	1055
Ser Ile Asn Glu Ile Gly Ser Ser Asp Glu Asn Ile Gln Ala Glu Leu		
1060	1065	1070
Gly Arg Asn Arg Gly Pro Lys Leu Asn Ala Met Leu Arg Leu Gly Val		
1075	1080	1085
Leu Gln Pro Glu Val Tyr Lys Gln Ser Leu Pro Gly Ser Asn Cys Lys		
1090	1095	1100
His Pro Glu Ile Lys Lys Gln Glu Tyr Glu Glu Val Val Gln Thr Val		
1105	1110	1115
112		
Asn Thr Asp Phe Ser Pro Tyr Leu Ile Ser Asp Asn Leu Glu Gln Pro		
1125	1130	1135
Met Gly Ser Ser His Ala Ser Gln Val Cys Ser Glu Thr Pro Asp Asp		
1140	1145	1150
Leu Leu Asp Asp Gly Glu Ile Lys Glu Asp Thr Ser Phe Ala Glu Asn		
1155	1160	1165
Asp Ile Lys Glu Ser Ser Ala Val Phe Ser Lys Ser Val Gln Arg Gly		
1170	1175	1180
Glu Leu Ser Arg Ser Pro Ser Pro Phe Thr His Thr His Leu Ala Gln		
1185	1190	1195
120		
Gly Tyr Arg Arg Gly Ala Lys Lys Leu Glu Ser Ser Glu Glu Asn Leu		
1205	1210	1215
Ser Ser Glu Asp Glu Glu Leu Pro Cys Phe Gln His Leu Leu Phe Gly		
1220	1225	1230
Lys Val Asn Asn Ile Pro Ser Gln Ser Thr Arg His Ser Thr Val Ala		
1235	1240	1245
Thr Glu Cys Leu Ser Lys Asn Thr Glu Glu Asn Leu Leu Ser Leu Lys		
1250	1255	1260
Asn Ser Leu Asn Asp Cys Ser Asn Gln Val Ile Leu Ala Lys Ala Ser		
1265	1270	1275
128		
Gln Glu His His Leu Ser Glu Glu Thr Lys Cys Ser Ala Ser Leu Phe		
1285	1290	1295
Ser Ser Gln Cys Ser Glu Leu Glu Asp Leu Thr Ala Asn Thr Asn Thr		
1300	1305	1310
Gln Asp Pro Phe Leu Ile Gly Ser Ser Lys Gln Met Arg His Gln Ser		
1315	1320	1325
Glu Ser Gln Gly Val Gly Leu Ser Asp Lys Glu Leu Val Ser Asp Asp		
1330	1335	1340
Glu Glu Arg Gly Thr Gly Leu Glu Glu Asn Asn Gln Glu Glu Gln Ser		
1345	1350	1355
136		
Met Asp Ser Asn Leu Gly Glu Ala Ala Ser Gly Cys Glu Ser Glu Thr		
1365	1370	1375
Ser Val Ser Glu Asp Cys Ser Gly Leu Ser Ser Gln Ser Asp Ile Leu		
1380	1385	1390

Thr Thr Gln Gln Arg Asp Thr Met Gln His Asn Leu Ile Lys Leu Gln  
 1395 1400 1405  
 Gln Glu Met Ala Glu Leu Glu Ala Val Leu Glu Gln His Gly Ser Gln  
 1410 1415 1420  
 Pro Ser Asn Ser Tyr Pro Ser Ile Ile Ser Asp Ser Ser Ala Leu Glu  
 1425 1430 1435 144  
 Asp Leu Arg Asn Pro Glu Gln Ser Thr Ser Glu Lys Ala Val Leu Thr  
 1445 1450 1455  
 Ser Gln Lys Ser Ser Glu Tyr Pro Ile Ser Gln Asn Pro Glu Gly Leu  
 1460 1465 1470  
 Ser Ala Asp Lys Phe Glu Val Ser Ala Asp Ser Ser Thr Ser Lys Asn  
 1475 1480 1485  
 Lys Glu Pro Gly Val Glu Arg Ser Ser Pro Ser Lys Cys Pro Ser Leu  
 1490 1495 1500  
 Asp Asp Arg Trp Tyr Met His Ser Cys Ser Gly Ser Leu Gln Asn Arg  
 1505 1510 1515 152  
 Asn Tyr Pro Ser Gln Glu Glu Leu Ile Lys Val Val Asp Val Glu Glu  
 1525 1530 1535  
 Gln Gln Leu Glu Ser Gly Pro His Asp Leu Thr Glu Thr Ser Tyr  
 1540 1545 1550  
 Leu Pro Arg Gln Asp Leu Glu Gly Thr Pro Tyr Leu Glu Ser Gly Ile  
 1555 1560 1565  
 Ser Leu Phe Ser Asp Asp Pro Glu Ser Asp Pro Ser Glu Asp Arg Ala  
 1570 1575 1580  
 Pro Glu Ser Ala Arg Val Gly Asn Ile Pro Ser Ser Thr Ser Ala Leu  
 1585 1590 1595 160  
 Lys Val Pro Gln Leu Lys Val Ala Glu Ser Ala Gln Gly Pro Ala Ala  
 1605 1610 1615  
 Ala His Thr Thr Asp Thr Ala Gly Tyr Asn Ala Met Glu Glu Ser Val  
 1620 1625 1630  
 Ser Arg Glu Lys Pro Glu Leu Thr Ala Ser Thr Glu Arg Val Asn Lys  
 1635 1640 1645  
 Arg Met Ser Met Val Val Ser Gly Leu Thr Pro Glu Glu Phe Met Leu  
 1650 1655 1660  
 Val Tyr Lys Phe Ala Arg Lys His His Ile Thr Leu Thr Asn Leu Ile  
 1665 1670 1675 168  
 Thr Glu Glu Thr Thr His Val Val Met Lys Thr Asp Ala Glu Phe Val  
 1685 1690 1695  
 Cys Glu Arg Thr Leu Lys Tyr Phe Leu Gly Ile Ala Gly Gly Lys Trp  
 1700 1705 1710  
 Val Val Ser Tyr Phe Trp Val Thr Gln Ser Ile Lys Glu Arg Lys Met  
 1715 1720 1725  
 Leu Asn Glu His Asp Phe Glu Val Arg Gly Asp Val Val Asn Gly Arg  
 1730 1735 1740  
 Asn His Gln Gly Pro Lys Arg Ala Arg Glu Ser Gln Asp Arg Lys Ile  
 1745 1750 1755 176  
 Phe Arg Gly Leu Glu Ile Cys Cys Tyr Gly Pro Phe Thr Asn Met Pro  
 1765 1770 1775  
 Thr Asp Gln Leu Glu Trp Met Val Gln Leu Cys Gly Ala Ser Val Val  
 1780 1785 1790  
 Lys Glu Leu Ser Ser Phe Thr Leu Gly Thr Gly Val His Pro Ile Val  
 1795 1800 1805  
 Val Val Gln Pro Asp Ala Trp Thr Glu Asp Asn Gly Phe His Ala Ile  
 1810 1815 1820  
 Gly Gln Met Cys Glu Ala Pro Val Val Thr Arg Glu Trp Val Leu Asp  
 1825 1830 1835 184  
 Ser Val Ala Leu Tyr Gln Cys Gln Glu Leu Asp Thr Tyr Leu Ile Pro

1845 1850 1855  
Gln Ile Pro His Ser His Tyr  
1860

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
AATCTTAGAG TGTCCCA 17

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
ATCTTAGTGT CCCACCT 17

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
CAGAAAAAAA GGTAGAT 17

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
CAGAAAAAAA AGGTAGA 17

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGAGAATCCC AGGACAG

17

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGAGAATCCC CAGGACA

17

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGGACCTGCG AAATCCA

17

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGGACCTGTG AAATCCA

17